



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/068,137A  
Source: 1600  
Date Processed by STIC: 4/5/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

**Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/068,137A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>    </u> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>    </u> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>    </u> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters; instead.	
4 <u>    </u> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u>    </u> Variable Length	Sequence(s) <u>        </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>    </u> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>        </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u>    </u> Skipped Sequences (OLD RULES)	Sequence(s) <u>        </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u>    </u> Skipped Sequences (NEW RULES)	Sequence(s) <u>        </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>    </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u>✓</u> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>    </u> Use of <220>	Sequence(s) <u>        </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>    </u> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>    </u> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



1600

## RAW SEQUENCE LISTING

DATE: 04/05/2004

PATENT APPLICATION: US/10/068,137A

TIME: 15:34:37

Input Set : A:\Sequence Listing 2-17-04 (copy to Examiner).txt

Output Set: N:\CRF4\04052004\J068137A.raw

2 <110> APPLICANT: Biopolo s.c.r.l.  
 3 <120> TITLE OF INVENTION: YEAST STRAINS FOR THE PRODUCTION OF LACTIC ACID  
 4 <130> FILE REFERENCE: 2027.547000  
 C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/068,137A  
 C--> 6 <141> CURRENT FILING DATE: 2002-02-06  
 7 <150> PRIOR APPLICATION NUMBER: ITALY MI97A002080  
 8 <151> PRIOR FILING DATE: 1997-12-09  
 9 <150> PRIOR APPLICATION NUMBER: PCT/EP98/05758  
 10 <151> PRIOR FILING DATE: 1998-09-11  
 11 <160> NUMBER OF SEQ ID NOS: 12  
 12 <170> SOFTWARE: PatentIn version 3.0  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 27  
 15 <212> TYPE: DNA  
 C--> 16 <213> ORGANISM: Artificial/Unknown *invalid <213> response*  
 17 <220> FEATURE:  
 18 <221> NAME/KEY: misc\_feature  
 19 <222> LOCATION: ()..()  
 20 <223> OTHER INFORMATION: Oligomer anneals to inactivated ampicillin resistance gene of  
 21 plasmid pALTER-1 and restores ampicillin resistance to mutant  
 22 strand after mutagenesis reaction *Insert a space between "pALTER-1" and "and"*  
 24 <400> SEQUENCE: 1  
 25 gttgccattg ctgcaggcat cgtggtg 27  
 29 <210> SEQ ID NO: 2  
 30 <211> LENGTH: 29  
 31 <212> TYPE: DNA  
 C--> 32 <213> ORGANISM: Artificial/Unknown *same error*  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: misc\_feature  
 35 <222> LOCATION: ()..()  
 36 <223> OTHER INFORMATION: Oligomer anneals upstream of Bos taurus LDH gene in 5'UTR and  
 37 creates XbaI restriction site 11 bp before start codon after  
 38 mutagenesis reaction  
 39 <400> SEQUENCE: 2  
 40 ccttttaggt ctagatccaa gatggcaac 29  
 44 <210> SEQ ID NO: 3  
 45 <211> LENGTH: 27  
 46 <212> TYPE: DNA  
 C--> 47 <213> ORGANISM: Artificial/Unknown  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: misc\_feature  
 50 <222> LOCATION: ()..()  
 51 <223> OTHER INFORMATION: Oligomer anneals to 5' end of L. casei LDH gene and  
 introduces a

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52      NcoI restriction site which changes the GTG start codon to an ATG
53      start codon
55 <400> SEQUENCE: 3
56 ccatggcaag tattacggat aaggatc          27
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 24
62 <212> TYPE: DNA
63 <213> ORGANISM: Lactobacillus casei
64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <222> LOCATION: ()..()
67 <223> OTHER INFORMATION: Antisense oligomer anneals 8 bp upstream of 3' end of L.
casei
68      LDH gene
70 <400> SEQUENCE: 4
71 ctatcactgc aggtttcga tgtc          24
75 <210> SEQ ID NO: 5
76 <211> LENGTH: 59
77 <212> TYPE: DNA
C--> 78 <213> ORGANISM: Artificial/Unknown
79 <220> FEATURE:
80 <221> NAME/KEY: misc_feature
81 <222> LOCATION: ()..()
82 <223> OTHER INFORMATION: Oligomer complementary to S. cerevisiae PDC1 and anneals to
83      loxP -KanSRD-loxP cassette
85 <400> SEQUENCE: 5
86 ttctactcat aacctcacgc aaaataacac agtcaaatca cagctgaagc ttcgtacgc          59
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 62
92 <212> TYPE: DNA
C--> 93 <213> ORGANISM: Artificial/Unknown
94 <220> FEATURE:
95 <221> NAME/KEY: misc_feature
96 <222> LOCATION: ()..()
97 <223> OTHER INFORMATION: Antisense oligomer complementary to S. cerevisiae PDC1 and
anneal
98      to loxP-KanSRD-loxP cassette
100 <400> SEQUENCE: 6
101 aatgcttata aaactttaac taataattag agattaaatc gcataggcca ctagtggatc          60
103 tg          62
107 <210> SEQ ID NO: 7
108 <211> LENGTH: 59
109 <212> TYPE: DNA
C--> 110 <213> ORGANISM: Artificial/Unknown
111 <220> FEATURE:
112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: ()..()
114 <223> OTHER INFORMATION: Oligomer complementary to S. cerevisiae PDC5 and anneals to
115      loxP -KanSRD-loxP cassette
117 <400> SEQUENCE: 7
118 atcaatctca aagagaacaa cacaatacaa taacaagaag cagctgaagc ttcgtacgc          59

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PATENT APPLICATION: US/10/068,137A

TIME: 15:34:37

Input Set : A:\Sequence Listing 2-17-04 (copy to Examiner).txt

Output Set: N:\CRF4\04052004\J068137A.raw

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122 <210> SEQ ID NO: 8
123 <211> LENGTH: 62
124 <212> TYPE: DNA
C--> 125 <213> ORGANISM: Artificial/Unknown
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: ()..()
129 <223> OTHER INFORMATION: Antisense oligomer complementary to S. cerevisiae PDC5 and
anneal to
130     to loxP-KanSRD-loxP cassette
132 <400> SEQUENCE: 8
133 aaaatacaca aacgttgaat catgagtttt atgttaatta gcataggcca ctagtggatc      60
135 tg                                                                    62
139 <210> SEQ ID NO: 9
140 <211> LENGTH: 59
141 <212> TYPE: DNA
C--> 142 <213> ORGANISM: Artificial/Unknown
143 <220> FEATURE:
144 <221> NAME/KEY: misc_feature
145 <222> LOCATION: ()..()
146 <223> OTHER INFORMATION: Oligomer complementary to S. cerevisiae PDC6 and anneals to
147     loxP-KanSRD-loxP cassette
149 <400> SEQUENCE: 9
150 taaataaaaa acccacgtaa tatagcaaaa acatattgcc cagctgaagc ttcgtacgc      59
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 62
156 <212> TYPE: DNA
C--> 157 <213> ORGANISM: Artificial/Unknown
158 <220> FEATURE:
159 <221> NAME/KEY: misc_feature
160 <222> LOCATION: ()..()
161 <223> OTHER INFORMATION: Antisense oligomer complementary to S. cerevisiae PDC6 and
anneals
162     to loxP-KanSRD-loxP cassette
164 <400> SEQUENCE: 10
165 ttattttgca acaataattc gtttgagtac actactaatg gcataggcca ctagtggatc      60
167 tg                                                                    62
171 <210> SEQ ID NO: 11
172 <211> LENGTH: 59
173 <212> TYPE: DNA
C--> 174 <213> ORGANISM: Artificial/Unknown
175 <220> FEATURE:
176 <221> NAME/KEY: misc_feature
177 <222> LOCATION: ()..()
178 <223> OTHER INFORMATION: Oligomer complementary to S. cerevisiae PDC2 and anneals to
179     loxP-KanSRD-loxP cassette
181 <400> SEQUENCE: 11
182 acgcaacttg aattggcaaa atgggcttat gagacgttcc cagctgaagc ttcgtacgc      59
186 <210> SEQ ID NO: 12
187 <211> LENGTH: 62
188 <212> TYPE: DNA

```

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Output Set: N:\CRF4\04052004\J068137A.raw

C--&gt; 189 &lt;213&gt; ORGANISM: Artificial/Unknown

190 &lt;220&gt; FEATURE:

191 &lt;221&gt; NAME/KEY: misc\_feature

192 &lt;222&gt; LOCATION: ()..()

193 <223> OTHER INFORMATION: Antisense oligomer complementary to S. cerevisiae PDC2 and  
anneals

194 to loxP-KanSRD-loxP cassette

196 &lt;400&gt; SEQUENCE: 12

197 agcctgtgtt accaggtaag tgtaagttat tagagtctgg gcataggcca ctagtggatc 60

199 tg 62

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/068,137A**

DATE: 04/05/2004

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Input Set : **A:\Sequence Listing 2-17-04 (copy to Examiner).txt**Output Set: **N:\CRF4\04052004\J068137A.raw**

L:5 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:32 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:47 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:78 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:93 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:110 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:125 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:142 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:157 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:174 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:189 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12